

SEQUENCE LISTING
Sub C2

(1) GENERAL INFORMATION:

(i) APPLICANT: Friedman, Jeffrey M.
Lee, Gwo-Hua
Proenca, Ricardo

(ii) TITLE OF INVENTION: DB, THE RECEPTOR FOR LEPTIN, NUCLEIC ACIDS ENCODING THE RECEPTOR, AND USES THEREOF

(iii) NUMBER OF SEQUENCES: 54

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: David A. Jackson, Esq.
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(C) CITY: Hackensack
(D) STATE: New Jersey
(E) COUNTRY: USA
(F) ZIP: 07601

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 14-FEBRUARY-1996
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 16-JANUARY-1996
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Jackson Esq., David A.
(B) REGISTRATION NUMBER: 26,742
(C) REFERENCE/DOCKET NUMBER: 600-1-162 CP1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 201-487-5800
(B) TELEFAX: 201-343-1684

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2821 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
CODING REGION: 1-2682

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: A15 (OB-Ra)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGATGTGTC AGAAATTCTA TGTGGTTTG TTACACTGGG AATTTCTTTA TGTGATAGCT	60
GCACCTAACCC TGGCATATCC AATCTCTCCC TGGAAATTAA AGTTGTTTG TGGACCACCG	120
AACACAAACCG ATGACTCCTT TCTCTCACCT GCTGGAGCCC CAAACAATGC CTCGGCTTTG	180
AAGGGGGCTT CTGAAGCAAT TGTTGAAGCT AAATTTAATT CAAGTGGTAT CTACGTTCT	240
GAGTTATCCA AAACAGTCTT CCACTGTTGC TTTGGGAATG AGCAAGGTCA AAACTGCTCT	300
GCACTCACAG ACAACACTGA AGGGAAGACA CTGGCTTCAG TAGTGAAGGC TTCAGTTTT	360
CGCCAGCTAG GTGTAAACTG GGACATAGAG TGCTGGATGA AAGGGGACTT GACATTATTC	420
ATCTGTCATA TGGAGCCATT ACCTAAGAAC CCCTTCAAGA ATTATGACTC TAAGGTCCAT	480
CTTTTATATG ATCTGCCTGA AGTCATAGAT GATTGCCTC TGCCCCACT GAAAGACAGC	540
TTTCAGACTG TCCAATGCAA CTGCAGTCTT CGGGGATGTG AATGTATGT GCCGGTACCC	600
AGAGCCAAAC TCAACTACGC TCTTCTGATG TATTTGGAAA TCACATCTGC CGGTGTGAGT	660
TTTCAGTCAC CTCTGATGTC ACTGCAGCCC ATGCTGTTG TGAAACCCGA TCCACCCCTTA	720
GGTTTGCATA TGGAAGTCAC AGATGATGGT AATTTAAAGA TTTCTGGGA CAGCCAAACAA	780
ATGGCACCAT TTCCGCTTCA ATATCAGGTG AAATATTTAG AGAATTCTAC AATTGTAAGA	840
GAGGCTGCTG AAATTGTCTC AGCTACATCT CTGCTGGTAG ACAGTGTGCT TCCTGGATCT	900
TCATATGAGG TCCAGGTGAG GAGCAAGAGA CTGGATGGTT CAGGAGTCTG GAGTGACTGG	960
AGTCACCTC AAGTCTTAC CACACAAGAT GTTGTGTATT TTCCACCCAA AATTCTGACT	1020
AGTGTGGAT CGAATGCTTC TTTTCATTGC ATCTACAAAA ACGAAAACCA GATTATCTCC	1080
TCAAAACAGA TAGTTGGTG GAGGAATCTA GCTGAGAAAA TCCCTGAGAT ACAGTACAGC	1140
ATTGTGAGTG ACCGAGTTAG CAAAGTTACC TTCTCCAACC TGAAAGCCAC CAGACCTCGA	1200
GGGAAGTTTA CCTATGACGC AGTGTACTGC TGCAATGAGC AGGCGTGCCA TCACCGCTAT	1260
GCTGAATTAT ACGTGATCGA TGTCAATATC AATATATCAT GTGAAACTGA CGGGTACTTA	1320
ACTAAAATGA CTTGCAGATG GTCACCCAGC ACAATCCAAT CACTAGTGGG AAGCACTGTG	1380
CAGCTGAGGT ATCACAGGCG CAGCCTGTAT TGTCTGATA GTCCATCTAT TCATCCTACG	1440
TCTGAGCCCA AAAACTGCGT CTTACAGAGA GACGGCTTT ATGAATGTGT TTTCCAGCCA	1500
ATCTTTCTAT TATCTGGCTA TACAATGTGG ATCAGGATCA ACCATTCTTT AGGTTCACTT	1560
GACTCGCCAC CAACGTGTGT CCTTCCTGAC TCCGTAGTAA AACCACTACC TCCATCTAAC	1620
GTAAAAGCAG AGATTACTGT AAACACTGGA TTATTGAAAG TATCTGGGA AAAGCCAGTC	1680
TTTCCGGAGA ATAACCTTCA ATTCCAGATT CGATATGGCT TAAGTGGAAA AGAAATACAA	1740

TGGAAGACAC	ATGAGGTATT	CGATGCAAAG	TCAAAGTCTG	CCAGCCTGCT	GGTGTCAAGAC	1800
CTCTGTGCAG	TCTATGTGGT	CCAGGTTCGC	TGCCGGCGGT	TGGATGGACT	AGGATATTGG	1860
AGTAATTGGA	GCAGTCCAGC	CTATACGCTT	GTCATGGATG	TAAAAGTTCC	TATGAGAGGG	1920
CCTGAATTTT	GGAGAAAAAT	GGATGGGAC	GTTACTAAAA	AGGAGAGAAA	TGTCACCTTG	1980
CTTGAAAGC	CCCTGACGAA	AAATGACTCA	CTGTGTAGTG	TGAGGAGGTA	CGTGGTGAAG	2040
CATCGTACTG	CCCACAATGG	GACGTGGTCA	GAAGATGTGG	GAAATCGGAC	CAATCTCACT	2100
TTCCTGTGGA	CAGAACCCAGC	GCACACTGTT	ACAGTTCTGG	CTGTCAATTG	CCTCGGCGCT	2160
TCCCTTGTGA	ATTTAACCT	TACCTTCTCA	TGGCCCATGA	GTAAAGTGAG	TGCTGTGGAG	2220
TCACTCAGTG	CTTATCCCCT	GAGCAGCAGC	TGTGTCATCC	TTTCCTGGAC	ACTGTCACCT	2280
GATGATTATA	GTCTGTTATA	TCTGGTTATT	GAATGGAAGA	TCCTTAATGA	AGATGATGGA	2340
ATGAAGTGGC	TTAGAATTCC	CTCGAATGTT	AAAAAGTTTT	ATATCCACGA	TAATTTTATT	2400
CCCATCGAGA	AATATCAGTT	TAGTCTTAC	CCAGTATTAA	TGGAAGGAGT	TGGAAAACCA	2460
AAGATAATT	ATGGTTTCAC	CAAAGATGCT	ATCGACAAGC	AGCAGAATGA	CGCAGGGCTG	2520
TATGTCATTG	TACCCATAAT	TATTCCTCT	TGTGTCCTAC	TGCTCGGAAC	ACTGTTAATT	2580
TCACACCAGA	GAATGAAAAA	GTTGTTTGG	GACGATGTTTC	CAAACCCCAA	GAATTGTTCC	2640
TGGGCACAAG	GACTGAATT	CCAAAGAGAGA	ACGGACACTC	TTTGAAGTCT	CTCATGACCA	2700
CTACAGATGA	ACCCAATCTA	CCAACTTCCC	AACAGTCCAT	ACAATATTAG	AAGATGTTA	2760
CATTTGGATG	GAGGGAAACA	ACCCTAAACT	ATGGTTGAA	TGACTAAGAA	ATAACATTTG	2820
A						2821

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 894 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: OB-Ra

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Met	Cys	Gln	Lys	Phe	Tyr	Val	Val	Leu	Leu	His	Trp	Glu	Phe	Leu
1					5				10				15		

Tyr Val Ile Ala Ala Leu Asn Leu Ala Tyr Pro Ile Ser Pro Trp Lys
 20 25 30

Phe Lys Leu Phe Cys Gly Pro Pro Asn Thr Thr Asp Asp Ser Phe Leu
 35 40 45

Ser Pro Ala Gly Ala Pro Asn Asn Ala Ser Ala Leu Lys Gly Ala Ser
 50 55 60

Glu Ala Ile Val Glu Ala Lys Phe Asn Ser Ser Gly Ile Tyr Val Pro
 65 70 75 80

Glu Leu Ser Lys Thr Val Phe His Cys Cys Phe Gly Asn Glu Gln Gly
 85 90 95

Gln Asn Cys Ser Ala Leu Thr Asp Asn Thr Glu Gly Lys Thr Leu Ala
 100 105 110

Ser Val Val Lys Ala Ser Val Phe Arg Gln Leu Gly Val Asn Trp Asp
 115 120 125

Ile Glu Cys Trp Met Lys Gly Asp Leu Thr Leu Phe Ile Cys His Met
 130 135 140

Glu Pro Leu Pro Lys Asn Pro Phe Lys Asn Tyr Asp Ser Lys Val His
 145 150 155 160

Leu Leu Tyr Asp Leu Pro Glu Val Ile Asp Asp Ser Pro Leu Pro Pro
 165 170 175

Leu Lys Asp Ser Phe Gln Thr Val Gln Cys Asn Cys Ser Leu Arg Gly
 180 185 190

Cys Glu Cys His Val Pro Val Pro Arg Ala Lys Leu Asn Tyr Ala Leu
 195 200 205

Leu Met Tyr Leu Glu Ile Thr Ser Ala Gly Val Ser Phe Gln Ser Pro
 210 215 220

Leu Met Ser Leu Gln Pro Met Leu Val Val Lys Pro Asp Pro Pro Leu
 225 230 235 240

Gly Leu His Met Glu Val Thr Asp Asp Gly Asn Leu Lys Ile Ser Trp
 245 250 255

Asp Ser Gln Thr Met Ala Pro Phe Pro Leu Gln Tyr Gln Val Lys Tyr
 260 265 270

Leu Glu Asn Ser Thr Ile Val Arg Glu Ala Ala Glu Ile Val Ser Ala
 275 280 285

Thr Ser Leu Leu Val Asp Ser Val Leu Pro Gly Ser Ser Tyr Glu Val
 290 295 300

Gln Val Arg Ser Lys Arg Leu Asp Gly Ser Gly Val Trp Ser Asp Trp
 305 310 315 320

Ser Ser Pro Gln Val Phe Thr Thr Gln Asp Val Val Tyr Phe Pro Pro
 325 330 335

Lys Ile Leu Thr Ser Val Gly Ser Asn Ala Ser Phe His Cys Ile Tyr
 340 345 350

Lys Asn Glu Asn Gln Ile Ile Ser Ser Lys Gln Ile Val Trp Trp Arg

355	360	365
Asn Leu Ala Glu Lys Ile Pro Glu Ile Gln Tyr Ser Ile Val Ser Asp		
370	375	380
Arg Val Ser Lys Val Thr Phe Ser Asn Leu Lys Ala Thr Arg Pro Arg		
385	390	395
Gly Lys Phe Thr Tyr Asp Ala Val Tyr Cys Cys Asn Glu Gln Ala Cys		
405	410	415
His His Arg Tyr Ala Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile		
420	425	430
Ser Cys Glu Thr Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser		
435	440	445
Pro Ser Thr Ile Gln Ser Leu Val Gly Ser Thr Val Gln Leu Arg Tyr		
450	455	460
His Arg Arg Ser Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr		
465	470	475
Ser Glu Pro Lys Asn Cys Val Leu Gln Arg Asp Gly Phe Tyr Glu Cys		
485	490	495
Val Phe Gln Pro Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg		
500	505	510
Ile Asn His Ser Leu Gly Ser Leu Asp Ser Pro Pro Thr Cys Val Leu		
515	520	525
Pro Asp Ser Val Val Lys Pro Leu Pro Pro Ser Asn Val Lys Ala Glu		
530	535	540
Ile Thr Val Asn Thr Gly Leu Leu Lys Val Ser Trp Glu Lys Pro Val		
545	550	555
560		
Phe Pro Glu Asn Asn Leu Gln Phe Gln Ile Arg Tyr Gly Leu Ser Gly		
565	570	575
Lys Glu Ile Gln Trp Lys Thr His Glu Val Phe Asp Ala Lys Ser Lys		
580	585	590
Ser Ala Ser Leu Leu Val Ser Asp Leu Cys Ala Val Tyr Val Val Gln		
595	600	605
Val Arg Cys Arg Arg Leu Asp Gly Leu Gly Tyr Trp Ser Asn Trp Ser		
610	615	620
Ser Pro Ala Tyr Thr Leu Val Met Asp Val Lys Val Pro Met Arg Gly		
625	630	640
Pro Glu Phe Trp Arg Lys Met Asp Gly Asp Val Thr Lys Lys Glu Arg		
645	650	655
Asn Val Thr Leu Leu Trp Lys Pro Leu Thr Lys Asn Asp Ser Leu Cys		
660	665	670
Ser Val Arg Arg Tyr Val Val Lys His Arg Thr Ala His Asn Gly Thr		
675	680	685
Trp Ser Glu Asp Val Gly Asn Arg Thr Asn Leu Thr Phe Leu Trp Thr		
690	695	700

Glu Pro Ala His Thr Val Thr Val Leu Ala Val Asn Ser Leu Gly Ala
 705 710 715 720

Ser Leu Val Asn Phe Asn Leu Thr Phe Ser Trp Pro Met Ser Lys Val
 725 730 735

Ser Ala Val Glu Ser Leu Ser Ala Tyr Pro Leu Ser Ser Cys Val
 740 745 750

Ile Leu Ser Trp Thr Leu Ser Pro Asp Asp Tyr Ser Leu Leu Tyr Leu
 755 760 765

Val Ile Glu Trp Lys Ile Leu Asn Glu Asp Asp Gly Met Lys Trp Leu
 770 775 780

Arg Ile Pro Ser Asn Val Lys Lys Phe Tyr Ile His Asp Asn Phe Ile
 785 790 795 800

Pro Ile Glu Lys Tyr Gln Phe Ser Leu Tyr Pro Val Phe Met Glu Gly
 805 810 815

Val Gly Lys Pro Lys Ile Ile Asn Gly Phe Thr Lys Asp Ala Ile Asp
 820 825 830

Lys Gln Gln Asn Asp Ala Gly Leu Tyr Val Ile Val Pro Ile Ile Ile
 835 840 845

Ser Ser Cys Val Leu Leu Leu Gly Thr Leu Leu Ile Ser His Gln Arg
 850 855 860

Met Lys Lys Leu Phe Trp Asp Asp Val Pro Asn Pro Lys Asn Cys Ser
 865 870 875 880

Trp Ala Gln Gly Leu Asn Phe Gln Lys Arg Thr Asp Thr Leu
 885 890

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2914 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
 - CODING REGION: 1349-2845

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: A40 (OB-Rb)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCATTGAGA GTGCCAACGG GAAGGCTTAA TTAACCTTG GAANTGAGTC CGAAGAGTCT	60
GGAAGTNTGT AAGATGGAAG ATACTATACA AGATACTTCA GAGCTGTACA TTCTTCCAGG	120

GATGTAGGCT AGCAGTTATT TCATTAGTAT ATGTCTATT TAGAATGGGA AGAATTAGGA	180
AGATGAATGG AGCCTGTGTC TTTCACTACT CTCCCAGGAG GTTCCAGAAT AGCNAAAGTG	240
TCAGGCCAGAA TTCTTGAAGT CATAGACTGG AGTTAGAGAT GAACATAAGC TCATGTTAAC	300
CCTGGGTTAC TTCTTATCAT CCTTAATTG GAAAGCTAAC AGGGCCTAAC CATCAAGAAC	360
GTCCTGGAGG AAAGAATGTT TTTAACGCCA TTATTCAAGTC AAAGAAATTA AGACTTGAGA	420
GAAATGCTCA TTTCTTCTCT CATGATGGCT CCTTACACCT TACTTCTACC GTACGATCCA	480
TGNGGCCCTA CCCACCGCAGG ATACATGCAT CTATATGAGA GTGTCTNCCC CTTCTAACTC	540
AGAGACTCTT GTTCTAGTCT GTGNATAAAA ATTCAAGCTTG TGGAAGCTTT CTGAGGGGTT	600
GGCAGCATTG AATTTTACCT GCAATAGGTA AAGGTAATCT TTTGGGAAGT GAAGAGTGT	660
ATTAGACATT TCAGAAAGAA CAAACAGGAT TGGGGCTGCT ATGTGTTCTA CACAGGAATC	720
TTCCATAACA CAGAATAATT TATGTAGATA GAGACAAGAT GGAAATGCC AGGGCCCCAA	780
AATAGCCGCT GTTATTTGTT AACCTTCAAG GTTTCTGTT TGTTTATCTG TTTCTTGCC	840
AGGATCATCT TCCAAGCACA TCCTGGGGGA ACAGTGGCAG AGTCACTCGA GTTCATGAAA	900
CTATGGTGAC ATCTGAGCTT CCTTGGTTCT TCACAGAACAA TAAGCAGTTC CTTTGCTTGC	960
TTGTTAGATG AGAAAACCTTC CTTGTCAGTC TGTCTCTACG ACTAGAATGG AAAGCCTTAC	1020
TACTTCCTAT GTATTCTAA TATTCAAAT GTCCTAATT TGTTTGGCTT CTCTGTCTTT	1080
AAGGGATTAA GTCTCTGGAT TTGAAGAAAT AAATAAATAA ATAAAGGAAA ACTAATTTTC	1140
TCGTGCCGGA TGACTGCTAG CTGAGCTCAG GCCTACTGCA TTCTACATTT CGACTCTCTC	1200
CCTCTTCCCC AGTGCTTAG CACTGGACTG GGCAGTNCC GGCCTGGTCT AACTCCTGTT	1260
TCCTGGTGGG AATGTATAAT AAGAACTCCA TGAGTTCTGG TATAAACACT GTGGTCTGTG	1320
TGCTAATTAA ATCTNGTGT TCCTACAGCC CCTGACGAAA AATGACTCAC TGTGTAGTGT	1380
GAGGAGGTAC GTGGTGAAGC ATCGTACTGC CCACAATGGG ACGTGGTCAG AAGATGTGGG	1440
AAATCGGACC AATCTCACTT TCCTGTGGAC AGAACCCAGCG CACACTGTTA CAGTTCTGGC	1500
TGTCAATTCC CTCGGCGCTT CCCTTGAA TTTAACCTT ACCTTCTCAT GGCCCATGAG	1560
TAAAGTGAGT GCTGTGGAGT CACTCAGTGC TTATCCCCCTG AGCAGCAGCT GTGTCACTCCT	1620
TTCCCTGGACA CTGTCACCTG ATGATTATAG TCTGTTATAT CTGGTTATTG AATGGAAGAT	1680
CCTTAATGAA GATGATGGAA TGAAGTGGCT TAGAATTCCC TCGAATGTTA AAAAGTTTA	1740
TATCCACGAT AATTTTATTC CCATCGAGAA ATATCAGTTT AGTCTTACCA CAGTATTAT	1800
GGAAGGAGTT GGAAAACCAA AGATAATTAA TGGTTTCACC AAAGATGCTA TCGACAAGCA	1860
GCAGAATGAC GCAGGGCTGT ATGTCATTGT ACCCATAATT ATTTCCCTT GTGTCTACT	1920
GCTCGGAACA CTGTTAATT CACACCAGAG AATGAAAAAG TTGTTTGGG ACGATGTTCC	1980
AAACCCCAAG AATTGTTCCCT GGGCACAGG ACTGAATTTC CAAAAGCCTG AAACATTGAA	2040
GCATTTTTT ACCAAGCATG CAGAATCAGT GATATTTGGT CCTCTTCTTC TGGAGCCTGA	2100

ACCCATTCA	GAAGAAATCA	GTGTCGATA	AGCTTGGAAA	AATAAAGATG	AGATGGTCCC	2160
AGCAGCTATG	GTCTCCCTTC	TTTGACCAC	ACCAGACCT	GAAAGCAGTT	CTATTTGTAT	2220
TAGTGACCA	TGTAACAGTG	CTAACTTCTC	TGGGTCTCAG	AGCACCCAGG	TAACCTGTGA	2280
GGATGAGTGT	CAGAGACAAC	CCTCAGTTAA	ATATGCAACT	CTGGTCAGCA	ACGATAAACT	2340
AGTGGAAACT	GATGAAGAGC	AAGGGTTTAT	CCATAGTCCT	GTCAGCAACT	GCATCTCCAG	2400
TAATCATTCC	CCACTGAGGC	AGTCTTCTC	TAGCAGCTCC	TGGGAGACAG	AGGCCAGAC	2460
ATTTTCCTT	TTATCAGACC	AGCAACCCAC	CATGATTCA	CCACAACTTT	CATTCTCGGG	2520
GTTGGATGAG	CTTTGGAAC	TGGAGGGAAG	TTTCCTGAA	GAAAATCACA	GGGAGAAAGTC	2580
TGTCTGTTAT	CTAGGAGTCA	CCTCCGTCAA	CAGAAGAGAG	AGTGGTGTGC	TTTGACTGG	2640
TGAGGCAGGA	ATCCTGTGCA	CATTCCCAGC	CCAGTGTCTG	TTCAGTGACA	TCAGGATCCT	2700
CCAGGAGAGA	TGCTCACACT	TTGTAGAAAA	TAATTTGAGT	TTAGGGACCT	CTGGTGAGAA	2760
CTTTGTACCT	TACATGCC	AATTCAAAC	CTGTTCCACG	CACAGTCACA	AGATAATGGA	2820
GAATAAGATG	TGTGACTTAA	CTGTGTAATC	TCATCCAAGA	AGCCTCAAGG	TTCCATTCCA	2880
GTAGAGCCTG	TCATGTATAA	TGTGTTCTTT	ATTG			2914

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 499 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: OB-Rb

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Pro	Leu	Thr	Lys	Asn	Asp	Ser	Leu	Cys	Ser	Val	Arg	Arg	Tyr	Val	Val
1							5			10				15	

Lys	His	Arg	Thr	Ala	His	Asn	Gly	Thr	Trp	Ser	Glu	Asp	Val	Gly	Asn
				20				25					30		

Arg	Thr	Asn	Leu	Thr	Phe	Leu	Trp	Thr	Glu	Pro	Ala	His	Thr	Val	Thr
			35			40							45		

Val	Leu	Ala	Val	Asn	Ser	Leu	Gly	Ala	Ser	Leu	Val	Asn	Phe	Asn	Leu
			50			55						60			

Thr	Phe	Ser	Trp	Pro	Met	Ser	Lys	Val	Ser	Ala	Val	Glu	Ser	Leu	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

65	70	75	80
Ala	Tyr	Pro	Leu
Ser	Ser	Ser	Cys
85	90	95	
Ile	Leu	Ser	Trp
Tyr	Leu	Val	Thr
100	105	110	Leu
Asn	Glu	Asp	Asp
Gly	Met	Lys	Trp
115	120	125	Arg
Lys	Phe	Tyr	Ile
130	135	140	His
Asp	Asn	Phe	Ile
145	150	155	Pro
Ser	Leu	Tyr	Ile
160	165	170	Glu
Asn	Gly	Phe	Thr
175	180	185	Lys
Leu	Tyr	Val	Ile
190	195	200	Val
Gly	Thr	Leu	Ile
205	210	215	Ser
Asp	Val	Pro	Asn
220	225	230	Pro
Gln	Lys	Pro	Glu
240	245	250	Thr
Val	Ile	Phe	Gly
255	260	265	Pro
Ile	Ser	Val	Asp
270	275	280	Thr
Ala	Met	Val	Ser
285	290	295	Leu
Ile	Cys	Ile	Ser
300	305	310	Asp
Ser	Thr	Gln	Val
320	325	330	Thr
Lys	Tyr	Ala	Thr
335	340	345	Leu
Glu	Gln	Gly	Phe
350	355	360	Ile
His	Ser	Pro	Leu
365	370	375	Arg
Ala	Gln	Thr	Phe
380	385	390	Leu
Pro	Gln	Leu	Ser
400	405	395	Phe
Ser	Phe	Pro	Glu
415	410	405	Glu
			Asn
			Arg
			Gly

Val Thr Ser Val Asn Arg Arg Glu Ser Gly Val Leu Leu Thr Gly Glu
 420 425 430
 Ala Gly Ile Leu Cys Thr Phe Pro Ala Gln Cys Leu Phe Ser Asp Ile
 435 440 445
 Arg Ile Leu Gln Glu Arg Cys Ser His Phe Val Glu Asn Asn Leu Ser
 450 455 460
 Leu Gly Thr Ser Gly Glu Asn Phe Val Pro Tyr Met Pro Gln Phe Gln
 465 470 475 480
 Thr Cys Ser Thr His Ser His Lys Ile Met Glu Asn Lys Met Cys Asp
 485 490 495
 Leu Thr Val

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1240 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
 - CODING REGION: 272-958
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: A6 (OB-Rc)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTTAAGGGAT TTAGTCTCTG GATTGAAGA AATAAATAAA TAAATAAAGG AAAACTAATT	60
TTCTCGTGCC GGATGACTGC TAGCTGAGCT CAGGCCTACT GCATTCTACA TTTGACTCT	120
CTCCCTCTTC CCCAGTGCTT TAGCACTGGA CTGGGCAGTN CCTGGCCTGG TCTAACTCCT	180
GTTTCCCTGGT GGGAAATGTAT AATAAGAACT CCATGAGTTC TGGTATAAAC ACTGTGGTCT	240
GTGTGCTAAT TAAATCTNGT GTTCCCTACA GCCCCTGACG AAAAATGACT CACTGTGTAG	300
TGTGAGGAGG TACGTGGTGA AGCATCGTAC TGCCCACAAT GGGACGTGGT CAGAAGATGT	360
GGGAAATCGG ACCAATCTCA CTTTCCTGTG GACAGAACCA GCGCACACTG TTACAGTTCT	420
GGCTGTCAAT TCCCTCGGCG CTTCCCTGTG GAATTAAAC CTTACCTTCT CATGGCCCAT	480
GAGTAAAGTG AGTGCCTGTGG AGTCACTCAG TGCTTATCCC CTGAGCAGCA GCTGTGTCT	540
CCTTTCCTGG ACACGTAC CTGATGATTA TAGTCTGTTA TATCTGGTTA TTGAATGGAA	600
GATCCTTAAT GAAGATGATG GAATGAAGTG GCTTAGAATT CCCTCGAATG TTAAAAAGTT	660
TTATATCCAC GATAATTAA TTCCCATCGA GAAATATCAG TTTAGTCTTT ACCCAGTATT	720

TATGGAAGGA	GTTGGAAAAC	CAAAGATAAT	TAATGGTTTC	ACCAAAAGATG	CTATCGACAA	780
GCAGCAGAAT	GACGCAGGGC	TGTATGTCAT	TGTACCCATA	ATTATTCCT	CTTGTGTCCT	840
ACTGCTCGGA	ACACTGTTAA	TTTCACACCA	GAGAATGAAA	AAGTTGTTT	GGGACGATGT	900
TCCAAACCCC	AAGAATTGTT	CCTGGGCACA	AGGACTGAAT	TTCCAAAAGG	TCACTGTTA	960
AGTATTTAA	CCCAGATATC	TAAGGTTGCA	GTTCAGATGC	CACAGTACTT	ACAGATCTTT	1020
AAACAACTTT	AAAGGGCTTT	ATGTTGTTGT	GTTCATGTTC	TCAAGCCTGT	TCATCCTTTC	1080
TCTTCTCAA	AAGCTGGGTT	TGGGATTGTA	TCAGAGAAAA	CAAAGTTCGC	TCCCTTATCT	1140
CATGAGAGTT	GACAACACAT	CTATCTCTCT	TTCTGCTTAC	TGTACATAAA	AAAAATAAAT	1200
ACTACAAGAG	GAAGGAATGT	TATAGATGGA	GAATAGATAG			1240

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 229 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: OB-Rc

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Pro	Leu	Thr	Lys	Asn	Asp	Ser	Leu	Cys	Ser	Val	Arg	Arg	Tyr	Val	Val
1							5				10				15

Lys	His	Arg	Thr	Ala	His	Asn	Gly	Thr	Trp	Ser	Glu	Asp	Val	Gly	Asn
								20		25			30		

Arg	Thr	Asn	Leu	Thr	Phe	Leu	Trp	Thr	Glu	Pro	Ala	His	Thr	Val	Thr
						35		40					45		

Val	Leu	Ala	Val	Asn	Ser	Leu	Gly	Ala	Ser	Leu	Val	Asn	Phe	Asn	Leu
						50		55			60				

Thr	Phe	Ser	Trp	Pro	Met	Ser	Lys	Val	Ser	Ala	Val	Glu	Ser	Leu	Ser
							65	70			75				80

Ala	Tyr	Pro	Leu	Ser	Ser	Ser	Cys	Val	Ile	Leu	Ser	Trp	Thr	Leu	Ser
							85		90				95		

Pro	Asp	Asp	Tyr	Ser	Leu	Leu	Tyr	Leu	Val	Ile	Glu	Trp	Lys	Ile	Leu
							100		105				110		

Asn	Glu	Asp	Asp	Gly	Met	Lys	Trp	Leu	Arg	Ile	Pro	Ser	Asn	Val	Lys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

115	120	125	
Lys Phe Tyr Ile His Asp Asn Phe Ile Pro Ile Glu Lys Tyr Gln Phe			
130	135	140	
Ser Leu Tyr Pro Val Phe Met Glu Gly Val Gly Lys Pro Lys Ile Ile			
145	150	155	160
Asn Gly Phe Thr Lys Asp Ala Ile Asp Lys Gln Gln Asn Asp Ala Gly			
165	170		175
Leu Tyr Val Ile Val Pro Ile Ile Ile Ser Ser Cys Val Leu Leu Leu			
180	185		190
Gly Thr Leu Leu Ile Ser His Gln Arg Met Lys Lys Leu Phe Trp Asp			
195	200		205
Asp Val Pro Asn Pro Lys Asn Cys Ser Trp Ala Gln Gly Leu Asn Phe			
210	215		220
Gln Lys Val Thr Val			
225			

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2892 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
CODING REGION: 1-2700
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: A8 (OB-Rd)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGATGTGTC AGAAATTCTA TGTGGTTTG TTACACTGGG AATTTCTTTA TGTGATAGCT	60
GCACCTAACCC TGGCATATCC AATCTCTCCC TGGAAATTAA AGTTGTTTTG TGGACCACCG	120
AACACAACCG ATGACTCCTT TCTCTCACCT GCTGGAGCCC CAAACAATGC CTCGGCTTTG	180
AAGGGGGCTT CTGAAGCAAT TGTTGAAGCT AAATTTAATT CAAGTGGTAT CTACGTTCCCT	240
GAGTTATCCA AACACAGTCTT CCACTGTTGC TTTGGGAATG AGCAAGGTCA AAACTGCTCT	300
GCACTCACAG ACAACACTGA AGGGAAGACA CTGGCTTCAG TAGTGAAGGC TTCAGTTTT	360
CGCCAGCTAG GTGTAAACTG GGACATAGAG TGCTGGATGA AAGGGGACTT GACATTATT	420
ATCTGTCATA TGGAGCCATT ACCTAAGAAC CCCTTCAAGA ATTATGACTC TAAGGTCCAT	480
CTTTTATATG ATCTGCCTGA AGTCATAGAT GATTCGCCTC TGCCCCACT GAAAGACAGC	540

TTTCAGACTG	TCCAATGCAA	CTGCAGTCTT	CGGGGATGTG	AATGTCATGT	GCCGGTACCC	600
AGAGCCAAAC	TCAACTACGC	TCTTCTGATG	TATTTGGAAA	TCACATCTGC	CGGTGTGAGT	660
TTTCAGTCAC	CTCTGATGTC	ACTGCAGCCC	ATGCTGTTG	TGAAACCCGA	TCCACCCTTA	720
GGTTTGCATA	TGGAAGTCAC	AGATGATGGT	AATTTAAAGA	TTTCTGGGA	CAGCCAAACA	780
ATGGCACCAT	TTCCGCTTCA	ATATCAGGTG	AAATATTAG	AGAATTCTAC	AATTGTAAGA	840
GAGGCTGCTG	AAATTGTCTC	AGCTACATCT	CTGCTGGTAG	ACAGTGTGCT	TCCTGGATCT	900
TCATATGAGG	TCCAGGTGAG	GAGCAAGAGA	CTGGATGGTT	CAGGAGTCTG	GAGTGACTGG	960
AGTTCACCTC	AAGTCTTAC	CACACAAGAT	GTTGTGTATT	TTCCACCCAA	AATTCTGACT	1020
AGTGTGGAT	CGAATGCTTC	TTTCATTGC	ATCTACAAAAA	ACGAAAACCA	GATTATCTCC	1080
TCAAAACAGA	TAGTTGGTG	GAGGAATCTA	GCTGAGAAAAA	TCCCTGAGAT	ACAGTACAGC	1140
ATTGTGAGTG	ACCGAGTTAG	CAAAGTTACC	TTCTCCAACC	TGAAAGCCAC	CAGACCTCGA	1200
GGGAAGTTTA	CCTATGACGC	AGTGTACTGC	TGCAATGAGC	AGGCGTGCCA	TCACCGCTAT	1260
GCTGAATTAT	ACGTGATCGA	TGTCAATATC	AATATATCAT	GTGAAACTGA	CGGGTACTTA	1320
ACTAAAATGA	CTTGCAGATG	GTCACCCAGC	ACAATCCAAT	CACTAGTGGG	AAGCACTGTG	1380
CAGCTGAGGT	ATCACAGGCG	CAGCCTGTAT	TGTCCTGATA	GTCCATCTAT	TCATCCTACG	1440
TCTGAGCCCC	AAAACCTGCGT	CTTACAGAGA	GACGGCTTTT	ATGAATGTGT	TTTCCAGGCCA	1500
ATCTTCTAT	TATCTGGCTA	TACAATGTGG	ATCAGGATCA	ACCATTCTTT	AGGTTCACTT	1560
GACTCGCCAC	CAACGTGTGT	CCTTCCTGAC	TCCGTAGTAA	AACCACCTACC	TCCATCTAAC	1620
GTAAAAGCAG	AGATTACTGT	AAACACTGGA	TTATTGAAAG	TATCTGGGA	AAAGCCAGTC	1680
TTTCCGGAGA	ATAACCTTCA	ATTCCAGATT	CGATATGGCT	TAAGTGGAAA	AGAAATACAA	1740
TGGAAGACAC	ATGAGGTATT	CGATGCAAAG	TCAAAGTCTG	CCAGCCTGCT	GGTGTCAAGAC	1800
CTCTGTGCAG	TCTATGTGGT	CCAGGTTCGC	TGCCGGCGGT	TGGATGGACT	AGGATATTGG	1860
AGTAATTGGA	GCAGTCCAGC	CTATACGCTT	GTCATGGATG	TAAAAGTTCC	TATGAGAGGG	1920
CCTGAATTTT	GGAGAAAAAT	GGATGGGAC	GTTACTAAAAA	AGGAGAGAAA	TGTCACCTTG	1980
CTTGGAAAGC	CCCTGACGAA	AAATGACTCA	CTGTGTAGTG	TGAGGAGGTA	CGTGGTGAAG	2040
CATCGTACTG	CCCACAATGG	GACGTGGTCA	GAAGATGTGG	GAAATCGGAC	CAATCTCACT	2100
TTCCTGTGGA	CAGAACCAAGC	GCACACTGTT	ACAGTTCTGG	CTGTCAATT	CCTCGGCGCT	2160
TCCCTTGTGA	ATTTAACCT	TACCTTCTCA	TGGCCCATGA	GTAAAGTGAG	TGCTGTGGAG	2220
TCACTCAGTG	CTTATCCCCT	GAGCAGCAGC	TGTGTATCC	TTTCTGGAC	ACTGTCACCT	2280
GATGATTATA	GTCTGTTATA	TCTGGTTATT	GAATGGAAGA	TCCTTAATGA	AGATGATGGA	2340
ATGAAGTGGC	TTAGAATTCC	CTCGAATGTT	AAAAAGTTTT	ATATCCACGA	TAATTTTATT	2400
CCCATCGAGA	AATATCAGTT	TAGTCTTAC	CCAGTATTAA	TGGAAGGAGT	TGGAAAACCA	2460
AAGATAATTA	ATGGTTTCAC	CAAAGATGCT	ATCGACAAGC	AGCAGAATGA	CGCAGGGCTG	2520

TATGTCATTG TACCCATAAT TATTCCTCT TGTCCTAC TGCTCGAAC ACTGTTAATT	2580
TCACACCAGA GAATGAAAAA GTTGTGG GACGATGTT CAAACCCCAA GAATTGTTCC	2640
TGGGCACAAG GACTGAATT CCAAAAGGAT ATATCTTAC ATGAAGTTTT TATTTTCAGA	2700
TAGCCTCTGG CAGATTCTCA CTGTGGCCTG AGGCAGCCTG AAACATTGA GCATCTTTT	2760
ACCAAGCATG CAGAACAGT GATATTGGT CCTCTTCTTC TGGAGCCTGA ACCCATTCA	2820
GAAGAAATCA GTGTCGATAC AGCTTGAAA AATAAAGATG AGATGGTCCC AGCAGCTATG	2880
GTCTCCCTTC TT	2892

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 900 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: OB-Rd

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Met Cys Gln Lys Phe Tyr Val Val Leu Leu His Trp Glu Phe Leu	
1 5 10 15	

Tyr Val Ile Ala Ala Leu Asn Leu Ala Tyr Pro Ile Ser Pro Trp Lys	
20 25 30	

Phe Lys Leu Phe Cys Gly Pro Pro Asn Thr Thr Asp Asp Ser Phe Leu	
35 40 45	

Ser Pro Ala Gly Ala Pro Asn Asn Ala Ser Ala Leu Lys Gly Ala Ser	
50 55 60	

Glu Ala Ile Val Glu Ala Lys Phe Asn Ser Ser Gly Ile Tyr Val Pro	
65 70 75 80	

Glu Leu Ser Lys Thr Val Phe His Cys Cys Phe Gly Asn Glu Gln Gly	
85 90 95	

Gln Asn Cys Ser Ala Leu Thr Asp Asn Thr Glu Gly Lys Thr Leu Ala	
100 105 110	

Ser Val Val Lys Ala Ser Val Phe Arg Gln Leu Gly Val Asn Trp Asp	
115 120 125	

Ile Glu Cys Trp Met Lys Gly Asp Leu Thr Leu Phe Ile Cys His Met	
130 135 140	

Glu Pro Leu Pro Lys Asn Pro Phe Lys Asn Tyr Asp Ser Lys Val His
 145 150 155 160

Leu Leu Tyr Asp Leu Pro Glu Val Ile Asp Asp Ser Pro Leu Pro Pro
 165 170 175

Leu Lys Asp Ser Phe Gln Thr Val Gln Cys Asn Cys Ser Leu Arg Gly
 180 185 190

Cys Glu Cys His Val Pro Val Pro Arg Ala Lys Leu Asn Tyr Ala Leu
 195 200 205

Leu Met Tyr Leu Glu Ile Thr Ser Ala Gly Val Ser Phe Gln Ser Pro
 210 215 220

Leu Met Ser Leu Gln Pro Met Leu Val Val Lys Pro Asp Pro Pro Leu
 225 230 235 240

Gly Leu His Met Glu Val Thr Asp Asp Gly Asn Leu Lys Ile Ser Trp
 245 250 255

Asp Ser Gln Thr Met Ala Pro Phe Pro Leu Gln Tyr Gln Val Lys Tyr
 260 265 270

Leu Glu Asn Ser Thr Ile Val Arg Glu Ala Ala Glu Ile Val Ser Ala
 275 280 285

Thr Ser Leu Leu Val Asp Ser Val Leu Pro Gly Ser Ser Tyr Glu Val
 290 295 300

Gln Val Arg Ser Lys Arg Leu Asp Gly Ser Gly Val Trp Ser Asp Trp
 305 310 315 320

Ser Ser Pro Gln Val Phe Thr Thr Gln Asp Val Val Tyr Phe Pro Pro
 325 330 335

Lys Ile Leu Thr Ser Val Gly Ser Asn Ala Ser Phe His Cys Ile Tyr
 340 345 350

Lys Asn Glu Asn Gln Ile Ile Ser Ser Lys Gln Ile Val Trp Trp Arg
 355 360 365

Asn Leu Ala Glu Lys Ile Pro Glu Ile Gln Tyr Ser Ile Val Ser Asp
 370 375 380

Arg Val Ser Lys Val Thr Phe Ser Asn Leu Lys Ala Thr Arg Pro Arg
 385 390 395 400

Gly Lys Phe Thr Tyr Asp Ala Val Tyr Cys Cys Asn Glu Gln Ala Cys
 405 410 415

His His Arg Tyr Ala Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile
 420 425 430

Ser Cys Glu Thr Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser
 435 440 445

Pro Ser Thr Ile Gln Ser Leu Val Gly Ser Thr Val Gln Leu Arg Tyr
 450 455 460

His Arg Arg Ser Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr
 465 470 475 480

Ser Glu Pro Lys Asn Cys Val Leu Gln Arg Asp Gly Phe Tyr Glu Cys
 485 490 495

Val Phe Gln Pro Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg
 500 505 510
 Ile Asn His Ser Leu Gly Ser Leu Asp Ser Pro Pro Thr Cys Val Leu
 515 520 525
 Pro Asp Ser Val Val Lys Pro Leu Pro Pro Ser Asn Val Lys Ala Glu
 530 535 540
 Ile Thr Val Asn Thr Gly Leu Leu Lys Val Ser Trp Glu Lys Pro Val
 545 550 555 560
 Phe Pro Glu Asn Asn Leu Gln Phe Gln Ile Arg Tyr Gly Leu Ser Gly
 565 570 575
 Lys Glu Ile Gln Trp Lys Thr His Glu Val Phe Asp Ala Lys Ser Lys
 580 585 590
 Ser Ala Ser Leu Leu Val Ser Asp Leu Cys Ala Val Tyr Val Val Gln
 595 600 605
 Val Arg Cys Arg Arg Leu Asp Gly Leu Gly Tyr Trp Ser Asn Trp Ser
 610 615 620
 Ser Pro Ala Tyr Thr Leu Val Met Asp Val Lys Val Pro Met Arg Gly
 625 630 635 640
 Pro Glu Phe Trp Arg Lys Met Asp Gly Asp Val Thr Lys Lys Glu Arg
 645 650 655
 Asn Val Thr Leu Leu Trp Lys Pro Leu Thr Lys Asn Asp Ser Leu Cys
 660 665 670
 Ser Val Arg Arg Tyr Val Val Lys His Arg Thr Ala His Asn Gly Thr
 675 680 685
 Trp Ser Glu Asp Val Gly Asn Arg Thr Asn Leu Thr Phe Leu Trp Thr
 690 695 700
 Glu Pro Ala His Thr Val Thr Val Leu Ala Val Asn Ser Leu Gly Ala
 705 710 715 720
 Ser Leu Val Asn Phe Asn Leu Thr Phe Ser Trp Pro Met Ser Lys Val
 725 730 735
 Ser Ala Val Glu Ser Leu Ser Ala Tyr Pro Leu Ser Ser Cys Val
 740 745 750
 Ile Leu Ser Trp Thr Leu Ser Pro Asp Asp Tyr Ser Leu Leu Tyr Leu
 755 760 765
 Val Ile Glu Trp Lys Ile Leu Asn Glu Asp Asp Gly Met Lys Trp Leu
 770 775 780
 Arg Ile Pro Ser Asn Val Lys Lys Phe Tyr Ile His Asp Asn Phe Ile
 785 790 795 800
 Pro Ile Glu Lys Tyr Gln Phe Ser Leu Tyr Pro Val Phe Met Glu Gly
 805 810 815
 Val Gly Lys Pro Lys Ile Ile Asn Gly Phe Thr Lys Asp Ala Ile Asp
 820 825 830
 Lys Gln Gln Asn Asp Ala Gly Leu Tyr Val Ile Val Pro Ile Ile Ile
 835 840 845

Ser Ser Cys Val Leu Leu Leu Gly Thr Leu Leu Ile Ser His Gln Arg
 850 855 860
 Met Lys Lys Leu Phe Trp Asp Asp Val Pro Asn Pro Lys Asn Cys Ser
 865 870 875 880
 Trp Ala Gln Gly Leu Asn Phe Gln Lys Asp Ile Ser Leu His Glu Val
 885 890 895
 Phe Ile Phe Arg
 900

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2468 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
 CODING REGION: 1-2415

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: A20 (OB-Re)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGATGTGTC AGAAATTCTA TGTGGTTTG TTACACTGGG AATTTCTTA TGTGATAGCT	60
GCACCTAACCC TGGCATATCC AATCTCTCCC TGGAAATTAA AGTTGTTTG TGGACCACCG	120
AACACAAACCG ATGACTCCTT TCTCTCACCT GCTGGAGCCC CAAACAATGC CTCGGCTTG	180
AAGGGGGCTT CTGAAGCAAT TGTTGAAGCT AAATTTAATT CAAGTGGTAT CTACGTTCC	240
GAGTTATCCA AAACAGTCTT CCACTGTTGC TTTGGGAATG AGCAAGGTCA AAACTGCTCT	300
GCACTCACAG ACAACACTGA AGGGAAGACA CTGGCTTCAG TAGTGAAGGC TTCAGTTTT	360
CGCCAGCTAG GTGTAAACTG GGACATAGAG TGCTGGATGA AAGGGGACTT GACATTATTC	420
ATCTGTCATA TGGAGCCATT ACCTAAGAAC CCCTTCAAGA ATTATGACTC TAAGGTCCAT	480
CTTTTATATG ATCTGCCTGA AGTCATAGAT GATTCGCCTC TGCCCCCACT GAAAGACAGC	540
TTTCAGACTG TCCAATGCAA CTGCAGTCTT CGGGGATGTG AATGTCATGT GCCGGTACCC	600
AGAGCCAAAC TCAACTACGC TCTTCTGATG TATTTGGAAA TCACATCTGC CGGTGTGAGT	660
TTTCAGTCAC CTCTGATGTC ACTGCAGCCC ATGCTTGTG TGAAACCCGA TCCACCCCTTA	720
GGTTTGATA TGGAAAGTCAC AGATGATGGT AATTTAAAGA TTTCTGGGA CAGCCAAACAA	780
ATGGCACCAT TTCCGCTTCA ATATCAGGTG AAATATTTAG AGAATTCTAC AATTGTAAGA	840
GAGGCTGCTG AAATTGTCTC AGCTACATCT CTGCTGGTAG ACAGTGTGCT TCCTGGATCT	900
TCATATGAGG TCCAGGTGAG GAGCAAGAGA CTGGATGGTT CAGGAGTCTG GAGTGACTGG	960

AGTTCACCTC AAGTCTTAC CACACAAGAT GTTGTGTATT TTCCACCCAA AATTCTGACT	1020
AGTGTGGAT CGAATGCTTC TTTTCATTGC ATCTACAAAA ACGAAAACCA GATTATCTCC	1080
TCAAAACAGA TAGTTGGTG GAGGAATCTA GCTGAGAAAA TCCCTGAGAT ACAGTACAGC	1140
ATTGTGAGTG ACCGAGTTAG CAAAGTTACC TTCTCCAACC TGAAAGCCAC CAGACCTCGA	1200
GGGAAGTTA CCTATGACGC AGTGTACTGC TGCAATGAGC AGGCGTGCCA TCACCGCTAT	1260
GCTGAATTAT ACGTGATCGA TGTCAATATC AATATATCAT GTGAAACTGA CGGGTACTTA	1320
ACTAAAATGA CTTGCAGATG GTCACCCAGC ACAATCCAAT CACTAGTGGG AAGCACTGTG	1380
CAGCTGAGGT ATCACAGGCG CAGCCTGTAT TGTCCCTGATA GTCCATCTAT TCATCCTACG	1440
TCTGAGCCC AAAACTGCGT CTTACAGAGA GACGGCTTTT ATGAATGTGT TTTCCAGCCA	1500
ATCTTCTAT TATCTGGCTA TACAATGTGG ATCAGGATCA ACCATTCTTT AGGTTCACTT	1560
GACTGCCAC CAACGTGTGT CCTTCCTGAC TCCGTAGTAA AACCACTACC TCCATCTAAC	1620
GTAAAAGCAG AGATTACTGT AAACACTGGA TTATTGAAAG TATCTGGGA AAAGCCAGTC	1680
TTTCCGGAGA ATAACCTTCA ATTCCAGATT CGATATGGCT TAAGTGGAAA AGAAATACAA	1740
TGGAAGACAC ATGAGGTATT CGATGCAAAG TCAAAGTCTG CCAGCCTGCT GGTGTCAGAC	1800
CTCTGTGCAG TCTATGTGGT CCAGGTTCGC TGCCGGCGGT TGGATGGACT AGGATATTGG	1860
AGTAATTGGA GCAGTCCAGC CTATACGCTT GTCATGGATG TAAAAGTTCC TATGAGAGGG	1920
CCTGAATTT GGAGAAAAAT GGATGGGAC GTTACTAAAA AGGAGAGAAA TGTCACCTTG	1980
CTTTGGAAGC CCCTGACGAA AAATGACTCA CTGTGTAGTG TGAGGAGGTA CGTGGTGAAG	2040
CATCGTACTG CCCACAATGG GACGTGGTCA GAAGATGTGG GAAATCGGAC CAATCTCACT	2100
TTCCTGTGGA CAGAACCAAGC GCACACTGTT ACAGTTCTGG CTGTCAATTG CCTCGGCGCT	2160
TCCCTTGTGA ATTTAACCT TACCTTCTCA TGGCCCATGA GTAAAGTGAG TGCTGTGGAG	2220
TCACTCAGTG CTTATCCCCT GAGCAGCAGC TGTGTATCC TTTCTGGAC ACTGTCACCT	2280
GATGATTATA GTCTGTTATA TCTGGTTATT GAATGGAAGA TCCTTAATGA AGATGATGGA	2340
ATGAAGTGGC TTAGAATTCC CTCGAATGTT AAAAAGTTTT ATATCCACGG TATGTGTACT	2400
GTACTTTCA TGGATTAGTA TGACACTGTA GACTGGCAAT TCTGATAATA AATCATTAA	2460
TGACAACC	2468

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 805 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: OB-Re

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Met Cys Gln Lys Phe Tyr Val Val Leu Leu His Trp Glu Phe Leu
 1 5 10 15

Tyr Val Ile Ala Ala Leu Asn Leu Ala Tyr Pro Ile Ser Pro Trp Lys
 20 25 30

Phe Lys Leu Phe Cys Gly Pro Pro Asn Thr Thr Asp Asp Ser Phe Leu
 35 40 45

Ser Pro Ala Gly Ala Pro Asn Asn Ala Ser Ala Leu Lys Gly Ala Ser
 50 55 60

Glu Ala Ile Val Glu Ala Lys Phe Asn Ser Ser Gly Ile Tyr Val Pro
 65 70 75 80

Glu Leu Ser Lys Thr Val Phe His Cys Cys Phe Gly Asn Glu Gln Gly
 85 90 95

Gln Asn Cys Ser Ala Leu Thr Asp Asn Thr Glu Gly Lys Thr Leu Ala
 100 105 110

Ser Val Val Lys Ala Ser Val Phe Arg Gln Leu Gly Val Asn Trp Asp
 115 120 125

Ile Glu Cys Trp Met Lys Gly Asp Leu Thr Leu Phe Ile Cys His Met
 130 135 140

Glu Pro Leu Pro Lys Asn Pro Phe Lys Asn Tyr Asp Ser Lys Val His
 145 150 155 160

Leu Leu Tyr Asp Leu Pro Glu Val Ile Asp Asp Ser Pro Leu Pro Pro
 165 170 175

Leu Lys Asp Ser Phe Gln Thr Val Gln Cys Asn Cys Ser Leu Arg Gly
 180 185 190

Cys Glu Cys His Val Pro Val Pro Arg Ala Lys Leu Asn Tyr Ala Leu
 195 200 205

Leu Met Tyr Leu Glu Ile Thr Ser Ala Gly Val Ser Phe Gln Ser Pro
 210 215 220

Leu Met Ser Leu Gln Pro Met Leu Val Val Lys Pro Asp Pro Pro Leu
 225 230 235 240

Gly Leu His Met Glu Val Thr Asp Asp Gly Asn Leu Lys Ile Ser Trp
 245 250 255

Asp Ser Gln Thr Met Ala Pro Phe Pro Leu Gln Tyr Gln Val Lys Tyr
 260 265 270

Leu Glu Asn Ser Thr Ile Val Arg Glu Ala Ala Glu Ile Val Ser Ala
 275 280 285

Thr Ser Leu Leu Val Asp Ser Val Leu Pro Gly Ser Ser Tyr Glu Val
 290 295 300
 Gln Val Arg Ser Lys Arg Leu Asp Gly Ser Gly Val Trp Ser Asp Trp
 305 310 315 320
 Ser Ser Pro Gln Val Phe Thr Thr Gln Asp Val Val Tyr Phe Pro Pro
 325 330 335
 Lys Ile Leu Thr Ser Val Gly Ser Asn Ala Ser Phe His Cys Ile Tyr
 340 345 350
 Lys Asn Glu Asn Gln Ile Ile Ser Ser Lys Gln Ile Val Trp Trp Arg
 355 360 365
 Asn Leu Ala Glu Lys Ile Pro Glu Ile Gln Tyr Ser Ile Val Ser Asp
 370 375 380
 Arg Val Ser Lys Val Thr Phe Ser Asn Leu Lys Ala Thr Arg Pro Arg
 385 390 395 400
 Gly Lys Phe Thr Tyr Asp Ala Val Tyr Cys Cys Asn Glu Gln Ala Cys
 405 410 415
 His His Arg Tyr Ala Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile
 420 425 430
 Ser Cys Glu Thr Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser
 435 440 445
 Pro Ser Thr Ile Gln Ser Leu Val Gly Ser Thr Val Gln Leu Arg Tyr
 450 455 460
 His Arg Arg Ser Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr
 465 470 475 480
 Ser Glu Pro Lys Asn Cys Val Leu Gln Arg Asp Gly Phe Tyr Glu Cys
 485 490 495
 Val Phe Gln Pro Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg
 500 505 510
 Ile Asn His Ser Leu Gly Ser Leu Asp Ser Pro Pro Thr Cys Val Leu
 515 520 525
 Pro Asp Ser Val Val Lys Pro Leu Pro Pro Ser Asn Val Lys Ala Glu
 530 535 540
 Ile Thr Val Asn Thr Gly Leu Leu Lys Val Ser Trp Glu Lys Pro Val
 545 550 555 560
 Phe Pro Glu Asn Asn Leu Gln Phe Gln Ile Arg Tyr Gly Leu Ser Gly
 565 570 575
 Lys Glu Ile Gln Trp Lys Thr His Glu Val Phe Asp Ala Lys Ser Lys
 580 585 590
 Ser Ala Ser Leu Leu Val Ser Asp Leu Cys Ala Val Tyr Val Val Gln
 595 600 605
 Val Arg Cys Arg Arg Leu Asp Gly Leu Gly Tyr Trp Ser Asn Trp Ser
 610 615 620
 Ser Pro Ala Tyr Thr Leu Val Met Asp Val Lys Val Pro Met Arg Gly
 625 630 635 640

Pro Glu Phe Trp Arg Lys Met Asp Gly Asp Val Thr Lys Lys Glu Arg
 645 650 655
 Asn Val Thr Leu Leu Trp Lys Pro Leu Thr Lys Asn Asp Ser Leu Cys
 660 665 670
 Ser Val Arg Arg Tyr Val Val Lys His Arg Thr Ala His Asn Gly Thr
 675 680 685
 Trp Ser Glu Asp Val Gly Asn Arg Thr Asn Leu Thr Phe Leu Trp Thr
 690 695 700
 Glu Pro Ala His Thr Val Thr Val Leu Ala Val Asn Ser Leu Gly Ala
 705 710 715 720
 Ser Leu Val Asn Phe Asn Leu Thr Phe Ser Trp Pro Met Ser Lys Val
 725 730 735
 Ser Ala Val Glu Ser Leu Ser Ala Tyr Pro Leu Ser Ser Cys Val
 740 745 750
 Ile Leu Ser Trp Thr Leu Ser Pro Asp Asp Tyr Ser Leu Leu Tyr Leu
 755 760 765
 Val Ile Glu Trp Lys Ile Leu Asn Glu Asp Asp Gly Met Lys Trp Leu
 770 775 780
 Arg Ile Pro Ser Asn Val Lys Lys Phe Tyr Ile His Gly Met Cys Thr
 785 790 795 800
 Val Leu Phe Met Asp
 805

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: C-terminal
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: OB-Ra

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Asn Phe Gln Lys Arg Thr Asp Leu
 1 5

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 amino acids
 - (B) TYPE: amino acid

(C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: C-terminal
- (vii) IMMEDIATE SOURCE:
 (B) CLONE: OB-Rb

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Asn	Phe	Gln	Lys	Pro	Glu	Thr	Phe	Glu	Gln	Leu	Phe	Thr	Lys	His	Ala
1				5				10					15		
Glu	Ser	Val	Ile	Phe	Gly	Pro	Leu	Leu	Leu	Glu	Pro	Glu	Pro	Ile	Ser
	20						25					30			
Glu	Glu	Ile	Ser	Val	Asp	Thr	Ala	Trp	Lys	Asn	Lys	Asp	Glu	Met	Val
	35					40					45				
Pro	Ala	Ala	Met	Val	Ser	Leu	Leu	Trp	Thr	Thr	Pro	Asp	Pro	Glu	Ser
	50					55				60					
Ser	Ser	Ile	Cys	Ile	Ser	Asp	Gln	Cys	Asn	Ser	Ala	Asn	Phe	Ser	Gly
	65				70				75				80		
Ser	Gln	Ser	Thr	Gln	Val	Cys	Glu	Asp	Glu	Cys	Gln	Arg	Gln	Pro	Ser
		85					90					95			
Val	Lys	Tyr	Ala	Thr	Leu	Val	Ser	Asn	Asp	Lys	Leu	Val	Glu	Thr	Asp
	100					105					110				
Glu	Glu	Gln	Gly	Phe	Ile	His	Ser	Pro	Val	Ser	Asn	Cys	Ile	Ser	Ser
	115					120					125				
Asn	His	Ser	Pro	Leu	Arg	Gln	Ser	Phe	Ser	Ser	Ser	Ser	Trp	Glu	Thr
	130					135					140				
Glu	Ala	Gln	Thr	Phe	Phe	Leu	Leu	Ser	Asp	Gln	Gln	Pro	Thr	Met	Ile
	145				150					155			160		
Ser	Pro	Gln	Leu	Ser	Phe	Ser	Gly	Leu	Asp	Glu	Leu	Leu	Glu	Leu	Glu
	165					170					175				
Gly	Ser	Phe	Pro	Glu	Glu	Asn	His	Arg	Glu	Lys	Ser	Val	Cys	Tyr	Leu
	180					185					190				
Gly	Val	Thr	Ser	Val	Asn	Arg	Arg	Glu	Ser	Gly	Val	Leu	Leu	Thr	Gly
	195					200					205				
Glu	Ala	Gly	Ile	Leu	Cys	Thr	Phe	Pro	Ala	Gln	Cys	Leu	Phe	Ser	Asp
	210					215					220				
Ile	Arg	Ile	Leu	Gln	Glu	Arg	Cys	Ser	His	Phe	Val	Glu	Asn	Asn	Leu
	225					230					235				240
Ser	Leu	Gly	Thr	Ser	Gly	Glu	Asn	Phe	Gly	Pro	Tyr	Met	Pro	Gln	Phe
		245					250					255			

Gln Thr Cys Ser Thr His Ser His Lys Ile Met Glu Asn Lys Met Cys
 260 265 270

Asp Phe Thr Val
 275

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: C-terminal
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: OB-Rc

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asn Phe Gln Lys Val Thr Val
 1 5

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: C-terminal
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: OB-Rd

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Asn Phe Gln Lys Asp Ile Ser His Glu Val Phe Ile Phe Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

- (ii) MOLECULE TYPE: peptide
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (v) FRAGMENT TYPE: C-terminal
 (vii) IMMEDIATE SOURCE:
 (B) CLONE: OB-Re

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Phe Tyr Ile His Gly Met Cys Thr Val Leu Phe Met Asp
 1 5 10

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant
 (ii) MOLECULE TYPE: peptide
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (v) FRAGMENT TYPE: internal
 (vii) IMMEDIATE SOURCE:
 (B) CLONE: OB-Ra/db/db

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Pro Gln Lys Arg Thr Asp Thr Leu
 1 5

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant
 (ii) MOLECULE TYPE: peptide
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:
 (B) CLONE: OB-Rb/wt

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Pro Gln Lys Pro Glu Thr
 1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GATGGAGGGA AA

12

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GATGGAGGTA AA

12

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
 ATCTTGGGTT CTCTGAAGAA

20

- (2) INFORMATION FOR SEQ ID NO:21:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:
 GAGATTGTCA GTCACAGCCT C

21

- (2) INFORMATION FOR SEQ ID NO:22:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
 ATCTGAATTG GAATCAAATA CAC

23

- (2) INFORMATION FOR SEQ ID NO:23:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:
AAATCTGTTA TCCTTCTGAA AC

22

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:
ACACTGTTAA TTTCACACCA GAG

23

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:
AGTCATTCAA ACCATTAGTT TAGG

24

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TGGATAAACCTTGCTCTTC A

21

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TGAACACAAAC AACATAAAGC CC

22

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGCTCCCTC AGGGCCAC

18

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTGACTGAAT GAAGATGTAA TATAC

25

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

His	Arg	Arg	Ser	Leu	Tyr	Cys	Pro	Asp	Ser	Pro	Ser	Ile	His	Pro	Thr
1				5					10				15		
Ser Glu Pro Lys															
20															

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Gln	Arg	Met	Lys	Lys	Leu	Phe	Trp	Asp	Asp	Val	Pro	Asn	Pro	Lys	Asn
1				5						10			15		
Cys Ser Trp															

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 166 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TGTTATATCT GGTTATTGAA TGG

23

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CATTAAATGA TTTATTATCA GAATTGC

27

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Glu Pro Leu Pro Lys Asn Pro Phe Lys Asn Tyr Asp Ser Lys
1 5 10

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: 7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AGGGNAAGCG CCGAGGGAAT TGACAGCCAG AACTGTAACA GTGTGCGCTG GTTCTGTCCA	60
CAGGAAAGTG AGATTGGTCC GATTTCCAC ATCTTCTGAC CACGTCCCAT TGTGGGCAGT	120
ACGATGCTTC ACCACGTACC TCCTCACACT ACACAGTGAG TCATTT	166

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 320 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: 11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GGTGAAGCAT CGTACTGCCA ACAATGGGAC GTGGTCAGAA GATGTGGAA ATCGGACCAA	60
TCTCACTTTC CTGTGGACAG AACCAAGCGCA CACTGTTACA GTTCTGGCTG TCAATTCCCT	120
CGGCGTTCC CTTGTGAATT TTAACCTTAC CTTCTCATGG CCCATGAGTA AAGTGAGTGC	180
TGTGGAGTCA CTCAGTGCTT ATCCCCTGAG CAGCAGCTGT GTCATCCTTT CCTGGACACT	240
GTCACCTGAT GATTATAGTC TGTTATATCT GGTTATTGAA TGGAAGATCC TTAATGAAGA	300
TGATGGAATG AAGTGGCTTA	320

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 158 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: 42

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GATTACTGGA GATGCAGTTG CTGACAGGAC TATGGATAAA CCCTTGCTCT TCATCAGTTT	60
CCACTAGTTT ATCGTTGCTG ACCAGAGTTG CATATTTAAC TGAGGGTTGT CTCTGACACT	120
CATCCTCACCA GGTTACCTGG GTGCTCTGAG ACCCAGAG	158

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: 46

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AGAGAGATCC CTGACCCTAG TTAGATCTGT TTTCAGGCTC TGTGTTCATC TGATGTTCAAG	60
AAGTCAGCAA GGTTCTCATA TGTCTGAGT TAGTAAGATG TCTCAGGGTT CCCCCATCAG	120
CTAACAAACCA CTTTGACATG AGAAGGCAGA AAGTTAAAGA ACACTACTTG GTGTTTTACT	180
TAAAGATAACG AG	192

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 168 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: 58

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AGACTGACAA GGAAGTTTC TCATCTAACCA AGCAAGCAAA GGAACTGCTT ATGTNCTGTG	60
ANGAACCAAG GNAGCTCAGA TGTCACCATA GTCATCATGA ACTCGAGTGA CTCTGCCACT	120
GTTCCCCCAG GATGTGCTTG GANGATAATC CTGCGCAAGA AACAGATA	168

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 259 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vii) IMMEDIATE SOURCE:

- (B) CLONE: S3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

AGAATTATGA CTCTAAGGTC CATCTTTAT ATGATCTGCC TGAAGTCATA GATGATTTCGC	60
CTCTGCCCTT ACTGAAAGAC AGNTTTCAGA CTGTCCAATG NAACTGCAGT CTTGGGGAT	120
GTGAATGTCA TGTGCCAGTA CCCAGAGCCA AACTCAACTA CGCTCTTCTG ATGTATTTGG	180
NAATCACATC TGCCGGTGTG AGTTTCAGT CACCTCTGAT GTCACTGCAG CCCATGCTTG	240
TTGTGAAACC CGATCCACC	259

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 250 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vii) IMMEDIATE SOURCE:

- (B) CLONE: S14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTTCAACAAT TGGTTCAGAA GCCCCCTTCA AAGCCGAGGC ATTGTTGGG GCTCCAGCAG	60
GTGAGAGAAA GGAGTCATCG GTTGTGTCG GTGGTCCACA AAACAACTTA AATTTCCAGG	120
GAGAGATTGG ATATGCCAGG TTAAGTGCAG CTATCACATA AAGAAATTCC CAGTGTAAACA	180

AAACCACATA GANTTTCTAA CACATCATCT TTCTTCAGAG GTGTACACCT GGATTTCAG 240
AACGATTCCCT 250

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CCGAGGGAAAT TGACAGGCC 18

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTCACTGTGT AGTGTGAGGA GG 22

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TCCTGTGGAC AGAACCCAGC

19

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TGACACAGCT GCTGCTCAG

19

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GGTCTCAGAG CACCCAGGTA

20

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

X (D) OLOGY linear

(ii) MOLECULETYPE:cDNA

(iii) HYPOTHETICAINO

(iv) ANTI-SENSENO

(xi) SEQUENCEDESCRIPTIONSEQ ID NO:47:

AGAGAGATCCTGACCCTAGT

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AACTTTCTGC CTTCCCTTCTC ATGTCA

26

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TTTCTCATCT AACAAAGCAAG CA

22

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ATCTGTTTCT TGCGCAGGAT

20

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CATTGTTTGG GGCTCCAG

18

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

AATCGTTCTG CAAATCCAGG

20

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TGAAGTCATA GATGATT CGC C

21

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GTTCGTACCC GACGTCACTG

Sub C²
cont.